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CHICKPEA (*CICER ARIETINUM* L.) GENOTYPES EVALUATION FOR HIGH YIELD THROUGH MULTIVARIATE ANALYSIS

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SUMMARY

Assessment of crop accessions through yield components is the most popular way for selecting well-adapted and stable genotypes for certain growing conditions. Chickpea (*Cicer arietinum* L.) is an important food legume crop in Uzbekistan. The 71 chickpea genotypes received an evaluation for morphological and yield traits through principal component, cluster, and biplot analyses. Principal component analysis (PCA) estimated chickpea variables into two main components accounting for 76.32% of the total variation. In chickpea genotypes, the traits viz., plant height, number of pods per plant, pods weight per plant, number of seeds per plant, seed weight, and seed yield showed a positive relationship with the first component (PC-I). Seed yield and the number of branches showed a positive correlation with the second component (PC-II). Biplot analysis indicated a positive association of seed yield (SY) with the number of branches (Br), number of pods per plant (NPP), number of seeds per plant (SPP), seed weight (SW), pod weight (PW), yet a negative association with plant height (PH). The 36 winter and 35 spring chickpea genotypes underwent analysis, then clustered based on various yield traits. The chickpea genotypes grouped into six clusters used the cluster analysis. Genotypes in cluster I and cluster VI showed the highest grain yield whereas cluster II and cluster III included the taller genotypes found suitable for mechanical harvesting. These findings can serve beneficial in chickpea hybridization for yield improvement in future breeding programs.

Keywords: Chickpea (*Cicer arietinum* L.), winter and spring chickpea, principal component analysis, cluster and biplot analyses, morphological and yield traits

Key findings: Multivariate analyses revealed that studied chickpea accessions gained clustering based on their morphological traits. Statistical analysis of chickpeas can provide valuable information for future chickpea breeding programs..

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INTRODUCTION

Chickpea (*Cicer arietinum* L.) is the most essential food legume crop in Asia (India and Pakistan), Syria, Turkey, and North Africa. It serves as the second largest sown food legume, occupying 15% of the total pulse area globally (except soybean), and the third largest crop, with a productivity of around 15 million MT worldwide (CGIAR, 2021). The nutritional value of chickpeas can result from the highest protein content (17%–30%) and macro- and microelements (Wallace *et al*., 2016; Hegde *et al*., 2018).

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Chickpeas obtain sufficient nitrogen via their symbiotic relationship with nitrogen-fixing bacteria, which is crucial in supporting growth and grain production. Like other legumes, chickpea fixing nitrogen association with rhizobial strains in soils provides benefits not only to itself but also gives excellent nutrition to the rotational and intercropping crops by improving soil fertility and structure and decreasing soil erosion in the agricultural production system (Ahlawat *et al*., 2005; Miller and Holmes, 2005; Jamil *et al*., 2022). Among the global biotic and abiotic stresses, terminal drought and heat stress are the major proposals to produce drought-resistant chickpeas for warmer short-season and semi-arid environments (Edenhofer *et.al.,* IPCC 2014).

Despite the widespread cultivation of chickpeas in Uzbekistan, there lacks varieties resistant to drought, biotic, and abiotic factors and adapted to climatic conditions. It is necessary to select and create productive genotypes resistant to diseases and abiotic stress from the world chickpea germplasm (Hussain *et al*., 2022). Selecting fruitful and stable cultivars requires knowledge of the components of productivity and productivity laws. The selection of parental genotypes for the cross-hybridization program needs a basis not only on a single trait but also on the combination of closely associated yield-related traits (Dawson *et al*., 2012; Zaazaa *et al*., 2012). The higher yield of chickpeas depends on many factors, and each factor has its effect. However, a separate study for factor effects seems inadequate for complete analysis.

Multivariate analysis is a series of methods, i.e., principal component (PCA), cluster, and factor analyses used to study genotypic diversity. Utilizing these techniques can identify groups of genotypes that have beneficial traits for breeding, elucidate the variation patterns in genotypes, and recognize the relationship among the genotypes (Aliu *et al*., 2016). Principal component analysis (PCA) can transform several possibly correlated variables into a smaller number of variables in a group called principal components (Tsehaye and Fikre, 2020). Through cluster analysis (CA), the genotypes are grouped based on complex traits rather than one character (Brown-Guedira *et al*., 2000). Past studies revealed the clustering of 17 chickpea genotypes from different geographical origins, seed colors, and grain yields into eight groups (Dani and Murty, 1985).

Clustering the various genotypes according to genetic diversity makes for the convenience of breeding, with groupings based on the degree of genetic divergence among the genotypes. For this purpose, cluster analysis is one of the most reliable tools to assess the relative contribution of different traits – constituents to the total diversity, to quantify the degree of divergence, and to choose genetically diverse parental genotypes to generate desirable recombinants (Vus *et al*., 2020). Cluster analysis has widely served the breeding processes for assessing different crop genotypes and comparing their parameters. Past studies applied the cluster analysis for working with the basic breeding material of tomatoes (Evgenidis *et al*., 2011), for assessing the genetic diversity and selection of parental pairs in winter wheat accessions (Khodadadi *et al*., 2011), and with the addition of principal component analysis, for assessing the genetic diversity in wheat (Mecha *et al*., 2017).

Several past studies revealed the genetic diversity in chickpea genotypes through multivariate analysis (Muniraja *et al*., 2011; Malik *et al*., 2014; Tsehaye and Fikre, 2020; Halavath *et al*., 2021; Jameel *et al*., 2021). Peyman *et al.* (2018) studied the genetic diversity in various chickpea genotypes and grouped them into two main groups and four clusters. Tsehaye and Fikre (2020) assessed the genetic diversity in chickpea genotypes under the potential environment of North Gondar, Ethiopia, indicating the first four principal components accounted for 81.5% of the total variation. Halavath *et al*. (2021) determined the genetic variability and effects of biochemical, physiological, and yield-related traits on seed yield in chickpeas through principal component analysis, observing days to flowering and maturity, chlorophyll indices, and grain yield as the first four main components.

Global climatic instabilities have become the major causes of yield losses in chickpeas (Jameel *et al*., 2021). In chickpea breeding, one of the relevant objectives is increasing plant productivity under stressful conditions. The purpose of the recent research studied the genetic diversity of the chickpea genotypes by using multivariate analysis to help select prospective parental genotypes for hybridization. In the future, such diversity can further create new high-yielding chickpea genotypes through selective breeding programs.

MATERIALS AND METHODS

Breeding material and procedure

The experimental material consisted of 71 chickpea genotypes acquired from ICARDA International elite CIENS-20 spring and CIENW-19 winter nurseries (Table 1). The study came about in the crop season of 2020–2021 at the Durmon Experimental Field Station, Institute of Genetics and Plant Experimental Biology, Academy of Sciences of the Republic of Uzbekistan. The experiment employed a randomized complete block design (RCBD) with two replications using 60 cm spacing and four-row plots with four meters of row length. The plot size measured 0.6 m × 4 m rows (2.4 m^2). Sowing of winter chickpea genotypes ensued on 15 October 2020, with harvesting done on 20 June 2021. Meanwhile, the spring genotypes, sown on 22 February 2021, were harvested on 20-25 June 2021. Plants gained fertilizers with 35:70 kg NP ha^{-1} obtained from urea and triple superphosphate.

Data recorded and statistical analysis

Data recording on randomly selected plants took place on plant height (PH), the number of branches (Br), pods per plant (NPP), seeds per pod (SPP), 100-seed weight (HSW), seed weight (SW), and seed yield (SY). The calculation of descriptive statistics, cluster analysis, and principal component analysis (PCA) used ANOVA in STATGRAPHICS-19 software (https://www.statgraphics.com/). Performing cluster analysis used K-means clustering, while a tree diagram development based on Euclidean distances utilized Ward's method.

RESULTS AND DISCUSSION

Analysis of the agronomic traits of the studied genotypes showed the highest variations. Plant height ranged from 26.3 to 82.2 cm. The same variation also showed for other traits, including 100-seeds weight and grain yield. The average grain yield was 382.38 g $plot^{-1}$; however, some genotypes showed the highest yield (645 g $plot^{-1}$), whereas some genotypes with low yield (Table 2).

Principal component analysis

Principal component analysis (PCA) is a mathematical procedure that transforms the maximum number of correlated variables into a minimum number of uncorrelated variables called principal components (Miller and Holmes, 2005). The first principal component accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible. The eigenvalue is imperative to decide which principal components are significant for further study (Toker and Cagirgan, 2004). A trait with a coefficient of greater than 0.3 has a large enough effect, thus considered an important trait. A general rule considered traits having less than 0.2 coefficient value have no significant effect on the overall variation. The use of PCA study the kind of variation found in the selected population (Muniraja *et al*., 2011). In chickpeas, more PCA studies occurred on pure breeding lines like germplasm lines, while no reports exist on the segregating populations (Kumar *et al*., 2003; Muniraja *et al*., 2011; Malik *et al*., 2014; Aliu *et al*., 2016; Halavath *et al*., 2021).

The analysis of yield data of 71 chickpea genotypes used PCA. The PCA grouped the estimated chickpea variables into two main components. From a total of eight components, only two had eigenvalues > 1 and showed 76.32% variability (Table 3.). The other five components explained only 23.68% of the variation in the chickpea genotypes. The results showed that PC-I explained 54.6%, while PC-II explained 21.7% of the total variance among various yield-related traits. Past studies reported 69.69% of the total variability in 25 chickpea genotypes evaluated for 11 yield traits (Peyman *et al*., 2018). Halavath *et al*. (2021) also studied 25 chickpeas genotypes and indicated three main principal components, which showed maximum contribution to the total diversity.

The first principal component (PC-I) showed the highest positive loading for seed weight (0.460), pods weight per plant (0.451), number of pods per plant (0.429), the number of seeds per plant (0.417), plant height (0.274), seed yield (0.233), and 100-seed weight (0.201) but showed the highest negative loading for primary branches per plant (-0.232) (Table 4). Principal component two (PC-II) showed the highest positive loading for seed yield (0.476) and branches per plant (0.440), whereas it showed the highest negative response for plant height (-0.470), 100-seed weight (-0.467), and seed weight per plant (0.019). Past studies also indicated a positive contribution of seed yield, number of pods per plant, and secondary branches per plant with PC-I and a negative

Table 1. Chickpea genotypes used in the present study.

Code	Genotype name /pedigree	Code	Genotype name/pedigree
11101	X07 TH 87/FLIP 03-110CXGhab4	11201	X07 TH 87/FLIP 03-110CXGhab4
11102	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)	11202	X07 TH 77/FLIP 03-117CXILC191
11103	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)	11203	Malxotra (Local Check)
11104	X07 TH 72/FLIP 03-97CXILC482	11204	X07 TH 87/FLIP 03-110CXGhab4
11105	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)	11205	ILC482 (Long term check)
11106	X07 TH 87/FLIP 03-110CXGhab4	11206	X07 TH 87/FLIP 03-110CXGhab4
11107	X07 TH 77/FLIP 03-117CXILC191	11208	X07 TH 72/FLIP 03-97CXILC482
11108	X07 TH 77/FLIP 03-117CXILC191	11209	X07 TH 75/FLIP 03-113CXILC3279
11109	X07 TH 68/FLIP 03-80CXILC191	11210	X07 TH 75/FLIP 03-113CXILC3279
11110	X07 TH 73/FLIP 03-110CXILC605	11211	X07 TH 75/FLIP 03-113CXILC3279
11111	X07 TH 73/FLIP 03-110CXILC605	11212	X07 TH 75/FLIP 03-113CXILC3279
11112	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)	11213	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)
11113	X79TH101/ILC 523 X ILC 183 (Improved check)	11214	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)
11114	X89TH258/ (FLIP 85-122CXFLIP 82-150C)/FLIP 86-77C	11215	X07 TH 77/FLIP 03-117CXILC191
11115	ILC482 (Long term check)	11216	X07 TH 77/FLIP 03-117CXILC191
11116	X07 TH 77/FLIP 03-117CXILC191	11217	X79TH101/ILC 523 X ILC 183 (Improved check)
11117	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)	11218	X07 TH 72/FLIP 03-97CXILC482
11119	X07 TH 75/FLIP 03-113CXILC3279	11219	X07 TH 89/FLIP 03-113CXFLIP97-706C
11120	X07 TH 87/FLIP 03-110CXGhab4	11220	X07 TH 77/FLIP 03-117CXILC191
11121	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)	11221	X07 TH 72/FLIP 03-97CXILC482
11122	X07 TH 77/FLIP 03-117CXILC191	11222	X07 TH 68/FLIP 03-80CXILC191
11123	X07 TH 75/FLIP 03-113CXILC3279	11223	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)
11124	Malxotra (Local Check)	11224	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)
11125	X07 TH 75/FLIP 03-113CXILC3279	11225	X89TH258/ (FLIP 85-122CXFLIP 82-150C)/FLIP86-77C
11126	X07 TH 87/FLIP 03-110CXGhab4	11226	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)
11127	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)	11227	X85 TH143/ILC 629 x FLIP 82-144C
11128	X07 TH 72/FLIP 03-97CXILC482	11228	X07 TH 87/FLIP 03-110CXGhab4
11129	X07 TH 72/FLIP 03-97CXILC482	11229	X07 TH 77/FLIP 03-117CXILC191
11130	X07 TH 89/FLIP 03-113CXFLIP97-706C	11230	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)
11131	X07 TH 77/FLIP 03-117CXILC191	11231	X07 TH 73/FLIP 03-110CXILC605
11132	X07 TH 75/FLIP 03-113CXILC3279	11233	X07 TH 87/FLIP 03-110CXGhab4
11133	X07 TH 87/FLIP 03-110CXGhab4	11234	X07 TH 73/FLIP 03-110CXILC605
11134	X07 TH 77/FLIP 03-117CXILC191	11235	X07 TH 72/FLIP 03-97CXILC482
11135	X07 TH 72/FLIP 03-97CXILC482	11236	X07 TH 69/FLIP 03-84CXILC200
11136	X07 TH 69/FLIP 03-84CXILC200		

Table 2. Mean value of some yield traits of chickpea genotypes**.**

Yield traits	Sx	Sd	V%	Range
Plant height	64.32	11.03	17.00	26.30 - 82.20
Branches	3.09	0.68	22.13	1.80 - 5.00
Pods plant^{-1}	41.43	12.27	29.61	20.20 - 89.60
Pod weight	21.10	6.53	30.94	8.23 - 38.28
Seeds plant^{-1}	47.87	14.05	29.37	22.40 - 91.10
Seed weight plant^{-1}	15.99	4.85	30.35	6.25 - 29.61
100-grain weight	34.69	6.42	18.51	22.72 - 50.58
Grain yield	382.38	109.38	28.60	87.90 - 645.20

Sx = mean of traits; Sd = standard deviation

Table 3. Principal component analysis of chickpea genotypes.

Sources of variation	PC-I	PC-II
Eigenvalue	4.37097	1.73817
Total variance (%)	54.637	21.690
Cumulative variance (%)	54.637	76.327

Table 4. First two principal components for the estimated variables of chickpea genotypes.

Traits	PC-I	PC-II
Plant height	0.274955	-0.470696
Branches plant^{-1}	-0.232783	0.440971
Pods per plant	0.429675	0.23201
Pod weight plant^{-1}	0.451993	-0.0311262
Seeds plant^{-1}	0.417584	0.288831
Seed weight plant^{-1}	0.460175	0.019644
100-seed weight	0.201908	-0.467221
Grain yield	0.233215	0.476538

contribution of plant height with PC-IV and 100-seed weight with PC-I and PC-III (Malik *et al*., 2014). Peyman *et al*. (2018) findings also revealed a positive response to the number of seeds per plant with PC-III, the number of pods per plant with PC-II, and negative loading of 100-seed weight with PC-II.

The PC-I recognized the main components, i.e., the number and weight of pods per plant and the number and weight of seeds per plant, contributing to the diversity among the chickpea genotypes. According to the PC-II, some of the studied chickpea genotypes were relatively branchy and had a high number of pods showing the highest grain yield.

Biplot analysis

In the vector view of the biplot, a vector drawn from the origin of the biplot to each symbol of the traits makes for easy visualization of the relationship among the traits. If the biplot explains a suitable amount of the total variation, the correlation coefficient between any of the two characters can be approximated by the cosine of the angle between the vectors. Two characters are positively correlated if the angle between the vectors is < 90, negatively correlated if the angle is > 90, and independent if the angle is 90 (Yan and Kang, 2002; Yan and Rajcan, 2002).

Biplot analysis indicated a positive association of seed yield (SY) with the number of branches (Br), number of pods per plant (NPP), number of seeds per plant (SPP), seed weight (SW), pod weight (PW), but a negative association with plant height (PH) and 100-seed weight (HSW) (Figure 1). Similar results came from Peyman *et al*. (2018), who observed a positive correlation between seed yield and the number of pods per plant. Contrary to present results, Kumar *et al*. (2003) revealed a positive correlation between seed yield and plant height.

Cluster analysis

The 36 winter and 35 spring chickpea genotypes received statistical analysis and then clustered based on various yield traits: plant height, branches per plant, number of pods per plant, pod weight, seed weight per plant, number of seeds per plant), 100-seed weight, and seed yield. Cluster analysis grouped 71 chickpea genotypes into two main groups, A and B. Group A comprised 30 genotypes (93.4% of winter chickpeas) and was further divided into three clusters (I, II, and III). Group B compound 41 genotypes (78.1% spring chickpea), also divided into three clusters (IV, V, and VI) (Figure 2).

Cluster I contained 14.08% winter chickpea genotypes, except for one spring chickpea genotype (12101) with a maximum seed yield. In cluster I, the 10 genotypes are characterized by the higher number of branches (60.89), the number of pods per plant (69.66), pod weight per plant (29.13), and seed yield (499.8 g/m^2). In cluster I, genotype 11112 showed the highest seed yield (645.2 g/m^2) due to the higher number of pods and seeds per plant. Based on yield traits, cluster I combined the higher yield, large grain, and upright-growing chickpea genotypes. The traits—the number of seeds per plant and 100-seed weight—revealed the foremost traits that directly affect plant productivity and incise the genetic diversity of chickpeas (Table 5). Past studies exhibited that the number of seeds per plant, secondary branches, and plant height positively correlate with seed yield (Toker and Cagirgan, 2004; Zali *et al*., 2009, 2011). The number of seeds and pod weight per plant were the determining factors of the chickpea plant's performance (Thangwana and Ogola, 2012). Therefore, the chickpea yield improvement can result from choosing a genotype having a larger number of primary and secondary branches, a greater number of pods and seeds per plant, and a

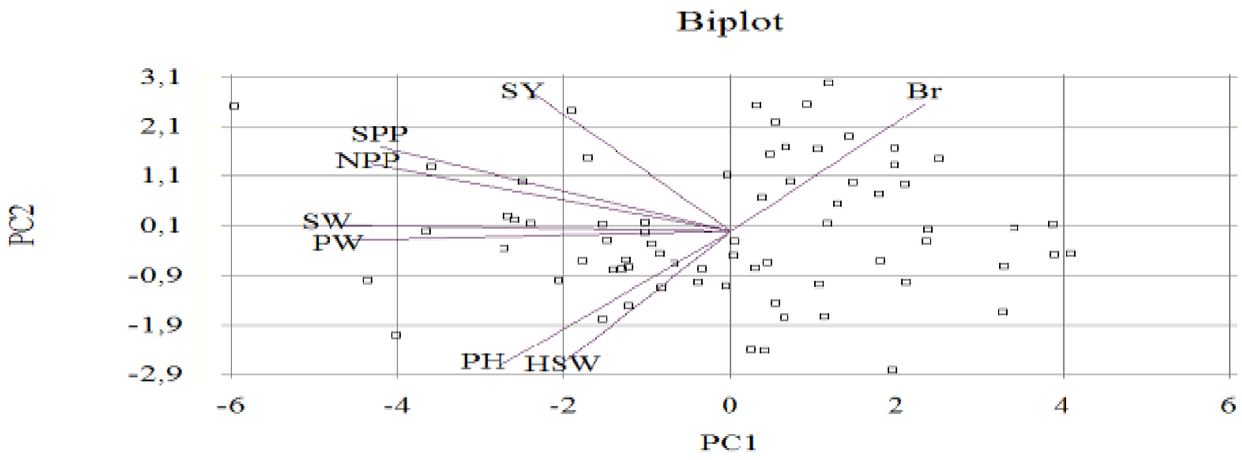

Figure 1. Biplot analysis of eight yield traits in various chickpea genotypes.

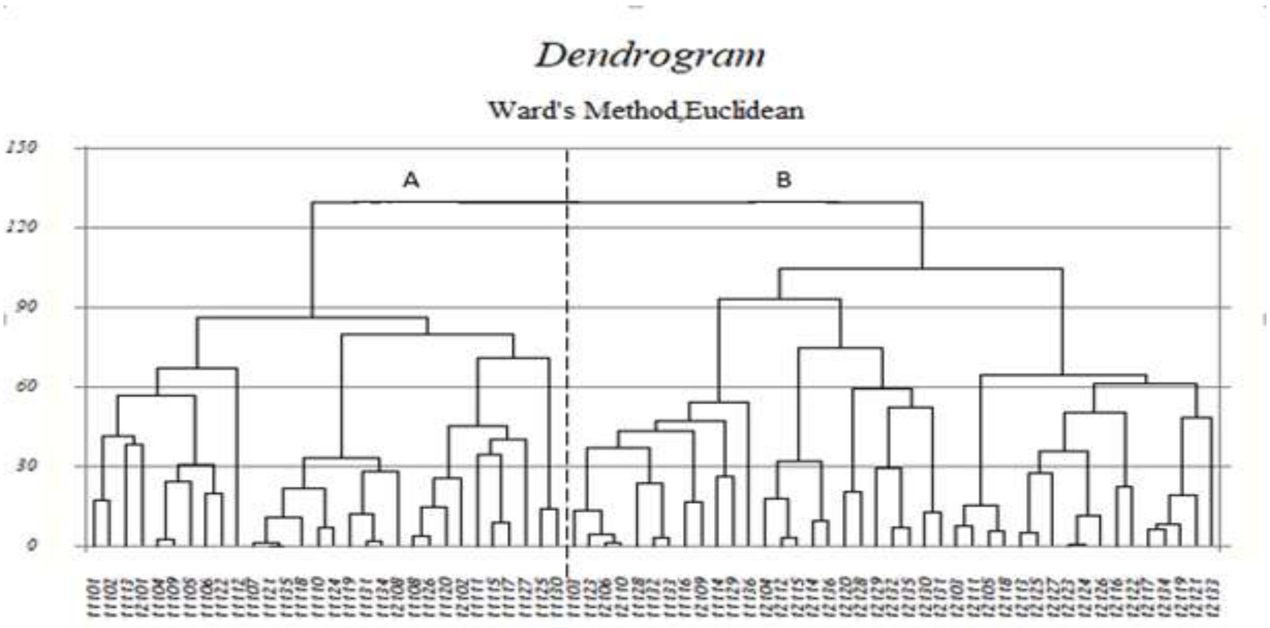

Figure 2. Tree diagram of 71 chickpea genotypes based on different yield traits.

higher 1000-seed weight (Wallace *et al*., 2016). The recent results also provided the possible selection of chickpea genotypes for higher yield potential under stress conditions.

Cluster II included winter chickpea genotypes with the highest number of seeds per plant (52.7) but a small value of 100-seed weight (33.43 g) and seed weight (17.68 g). Despite the small seed weight, the plants were taller (73.22 cm) (Table 5). Mechanical harvesting of chickpeas has a severe problem because of the crop height and header loss in combined harvesting (Basha *et al*., 2020). Therefore, the chickpea genotypes in cluster II will be suitable for mechanical harvesting.

Cluster III comprised 10 genotypes (90% winter chickpea), classified by the highest values of 100-seed weight (43.9 g) and grain yield (351.5 g), yet having moderate values for all the other traits. The registered largest mean value of 100-seed weight in the chickpea genotypes emerged in cluster III, with the smallest mean value obtained in cluster VI. In chickpea genotypes, the 100-seed weight displayed a close association with the grain yield (Gul *et al*., 2015).

Table 5. Descriptive statistics of the yield traits for 73 chickpea genotypes grouped under six clusters.

Traits	Clusters											
	Cluster I		Cluster II		Cluster III		Cluster IV		Cluster V		Cluster VI	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Plant height	69.52	2.73	73.22	1.59	71.18	2.06	70.30	2.66	58.39	1.69	51.98	4.2
Branches plant^{-1}	2.80	0.13	2.44	0.06	2.88	0.15	2.73	0.15	3.40	0.26	3.83	0.18
Pods per plant	60.89	3.82	45.41	1.30	47.78	2.05	36.63	1.98	25.72	1.68	38.41	1.94
Pod weight plant^{-1}	29.13	1.32	22.25	0.58	28.91	1.98	18.94	0.84	13.51	1.09	18	1.01
Seeds plant^{-1}	69.66	2.94	52.70	1.42	55.55	2.34	38.56	1.71	28.63	1.54	47.87	3.06
Seed weight plant^{-1}	22.49	0.88	17.68	0.24	21.00	1.35	14.25	0.64	9.66	0.62	13.94	0.73
100-seed weight	34.68	1.63	33.43	0.95	43.93	1.29	39.01	1.73	31.06	1.67	29.51	1.43
Grain yield	499.80	29.59	398.42	17.16	351.50	19.41	299.71	24.84	299.47	44.86	438.91	32.12

Cluster IV contained 12 genotypes (16.9%) comprising nine winter and three spring chickpea genotypes. These genotypes were characterized by a low number of seeds per plant but a higher value of a 100-seed weight (39.01 g) and plant height (70.3 cm). In Cluster IV, the decreased grain yield in genotypes may have resulted in a low number of productive pods and grains per pod (Table 5).

Cluster V contained only spring chickpea genotypes with a higher number of branches (3.4) but a low number of pods per plant (25.72), grain yield (299.47 g), and a low number of seeds per plant (28.63) (Table 5). This cluster carried closely related spring chickpea genotypes with lower seed yield and higher sensitivity to stress conditions. Past observations stated that the number of branches and pods, 100-seed weight, and grain yield revealed the highest coefficient of heritability (Tsehaye *et al*., 2020).

Cluster VI contains 23.9% of genotypes with a high number of branches, medium plant height, small grains, and the least 100-seed weight. Despite a higher number of seeds per plant, these chickpea genotypes have a high seed yield (438.91 g) among spring chickpeas. Chickpea genotypes 11135, 11106, 11119, and 11122 showed the highest grain yield compared with the control variety, 11124.

CONCLUSIONS

Characterizing the present chickpea (*Cicer arietinum* L.) genotypes revealed better genetic variability among the yield traits. According to the principal component and biplot analyses, the number of pods per plant, pod weight per plant, the number of seeds per plant, and seed weight per plant appeared as the main yield components that manage and improve the grain yield. Cluster analysis of chickpea genotypes indicated that genotypes in each cluster had some specific traits. The winter chickpea genotypes retained greater seed yield potential, with the genotypes in Cluster I and III utilized in future breeding programs. With genotypes grouped into one in cluster analysis, selecting high-yielding genotypes adapted to Uzbekistan conditions is convenient. The cluster analysis classified the chickpea genotypes into six groups, which could lead to selecting the high-yielding genotypes in the future breeding program.

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